

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

```
/tmp/fastaCAAQPaiHi: 995 aa  
>SEQ ID NO:2  
vs  /tmp/fastaDAARPaiHi library  
searching /tmp/fastaDAARPaiHi library
```

1008 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 39, opt: 27, gap-pen: -12/-2, width: 16

Scan time: 0.050

The best scores are: opt
NM 000096 ACCESSION:NM 000096 NID: gi 4557484 ref (1008) 2671

```
>>NM_000096 ACCESSION:NM_000096 NID: gi 4557484 ref NM_0 (1008 aa)
initn: 1414 init1: 972 opt: 2671
Smith-Waterman score: 3980; 57.002% identity in 1014 aa overlap (1-992:1-1008)
```

	10	20	30	40	50
SEQ	MKILILGIFLFLCSSPGWAIDRHCYIGIEESIWNYAPSGKNMLNEKPFSEDLE---	FLQ			
	::: ::::: ::::: ::::: :::	::: ::::: ::::: :::	::: ::::: :::	::: :::	::: :::
NM_000	MKILILGIFLFLCSTPAWAKEKHYIIGIIETTDY---	SDHGEKKLISVDTEHSNIYLQ			
	10	20	30	40	50

	60	70	80	90	100	110
SEQ	GGQARKSFVFKKALYFQYTDNTFQRRIIEKPSWLGFLGPMIKAETGDFIVYHVKNNASRAY					

NM_000	NGPDRIGRLYKKALYLQYTDFTRTTIEKPVWLGFGLGPIIKAETGDKVYVHLKNLASRPy					
	60	70	80	90	100	110

	120	130	140	150	160	170
SEQ	SYHPHGLTYSKENEAHGAIYPDNTTGLQKEVEYLEPGKQYT _{KWYVEEHQGP} GPNDSCNV					
	..	:	:	:	:	:
NM_000	TFHSHGITYYKEHE--GAIYPDNTTDFQRADDKVYPGEQYT _{YMLLATEEQSP} PGE _{GDGNCV}					
	120	130	140	150	160	170

300	310	320	330	340	350
SEQ	PVYLRGQTLISRNRKDTIMLFPSSLEDAFMVAKAPGVWMLGCQ---	IHESMQAFFKVS			
:..: ..:. : : : ..: .: ..: .: ..: ..: ..: ..: ..: ..: ..: ..: ..:				
NM_000	AAFFHGQALTNKNYRIDTINLFATLFDAYMVAQNPGGEWMLSCQNLNHLKAGLQAFFQVQ				

	360	370	380	390	400	410
SEQ	NCQKPSTEAFVTGTHVIHYYIAAKEILWNYAPSGIDFFTAKNLTAAGSKSQLFFERSPTR					
NM_000	ECNKSSSKDNIRGKHVRHYYIAAEEIIWNYAPSGIDIFTKENLTAPGSDSAVFFEQGTTR	360	370	380	390	400
						410
	420	430	440	450	460	
SEQ	IGGYKKLIYREYTDASFQTQKAR---EEHLGLGPVFKAEVGQTICKTIFYNNASLPLSI					
NM_000	IGGSYKKLVYREYTDASFTNRKERGPSEEHLGLGPVIWAEVGDTIRVTFHNGAYPLSI	420	430	440	450	460
						470
	470	480	490	500	510	520
SEQ	QPGLHYNKSNEGLFYE---TPGG-STPPPSHVSPGTTFVYTWEVPKDVGPTSTDPNCL					
NM_000	EPIGVRFNKNNEGTYYSNPYNPQSRSVPPSASHVAPTEFTYEWTVPKEVGPTNADPVCL	480	490	500	510	520
						530
	530	540	550	560	570	580
SEQ	TWFYYSSVNGKKDINSGLGPLLICRNGSLGDDGKQKGVDKEFYLLATIFDENESNLLDE					
NM_000	AKMYYSAVDPTKDIIFTGLIGPMKICKKGS LHANGRQKDVKEFYLFPTVFDENESLLLED	540	550	560	570	580
						590
	590	600	610	620	630	640
SEQ	N-RTFITEPENIDKEDTDCQASNKMY SINGYMYGNLPGLDTCLGDNVLWHVFSVGSVEDL					
NM_000	NIRMFTTAPDQVDKEDEDFQESNKMHSMNGFMYGNQPGLTMCKGDSVVWYLFSAGNEADV	600	610	620	630	640
						650
	650	660	670	680	690	700
SEQ	HGIYFSGNTFTSLGARRDTIPMF PYTSQTL MTPDSIGTFDLVCMTIKHNLGGMKHKYHV					
NM_000	HGIYFSGNTYLWRGERRD TANLF PQTSLTLHMWPDT EGTFNVECLTTDHYTGGMKQKYTV	660	670	680	690	700
						710
	710	720	730	740	750	760
SEQ	RQC GKP NPD QTQY QEEK III ITIAAEEMEW DYSPSRKWE NE LHH LRREN QTS MYVDRSGTL					
NM_000	NQC RRQ SED STF YLGERT YY -IAAVEVEWDY SPQ REWE KEL HHL QE QNV SNAFL DKG EFY	720	730	740	750	760
						770
	770	780	790	800	810	820
SEQ	LGSKYKKVLYRQYDDNTFTNQTKRNEGEKHL DIL GPL LILLNPGQIIQIIFKNKAARP YSI					
NM_000	I GS KYKKV VYRQY TDSTFR VPVERKAEE EHL GLGPQLHADVGDKV KIIFKNM ATR P YSI	780	790	800	810	820
						830
	830	840	850	860	870	880
SEQ	HAHGVKTNNSTVVPTQPGEIQIYTWQIPDRTGPTSLDFECIPWFY YSTVSVAKDLHSGLV					
NM_000	HAHGVQTESSTVTP TL PGETL TYVWK I PERSGAGTEDSACI PWAY YSTV DQVKD LYSG LI	840	850	860	870	880
						890

890 900 910 920 930
SEQ GPLSVCR----KDINPN-IVHRLVLHMIFDENESWYFEDSINTYASKPNKVDKENDNFQL
::: ::: : .: .. .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
NM_000 GPLIVCRRPYLKVNPRRKLEFALLFLVFDENESWYLDNNIKTYSDHPEKVNKDDEEFIE
900 910 920 930 940 950

940 950 960 970 980 990
SEQ SNQMHAINGRLFGNNQGITFHVGDVVNWLIGIGNEADLHTVHFHGHSFSEYKHKYLI
::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
NM_000 SNKMHAINGRMFGNLQGLTMHVGDEVNWYLMGMGNEIDLHTVHFHGHSFQYKHR
960 970 980 990 1000

995 residues in 1 query sequences

1008 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Wed Sep 18 11:16:31 2002 done: Wed Sep 18 11:16:32 2002

Scan time: 0.050 Display time: 1.417

Function used was FASTA